RAW SEQUENCE LISTING
ERROR REPORT

BIOTECH..JLOGY
SYSTEMS
BRANCH
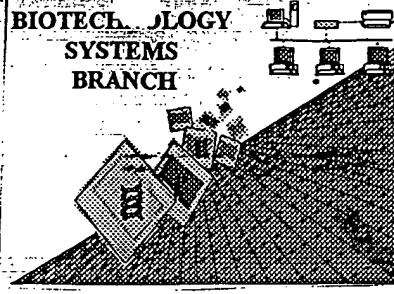
RECEIVED

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/522,727_

Source: _1644_

Date Processed by STIC: _1-04-01_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION   SERIAL NUMBER: 09/522,727

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 ✓ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

RAW SEQUENCE LISTING   DATE: 01/04/2001
PATENT APPLICATION: US/09/522,727   TIME: 08:52:41

Input Set : A:\47577.txt
Output Set: N:\CRF3\01042001\I522727.raw

```
    4 <110> APPLICANT: DANA-FARBER CANCER INSTITUTE, INC.
    5        MARASCO, Wayne
    6        MHASHILKAR, Abner
    8 <120> TITLE OF INVENTION: INTRABODY-MEDIATED CONTROL OF IMMUNE
    9        REACTIONS
   11 <130> FILE REFERENCE: 47577 CA
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/522,727
C--> 14 <141> CURRENT FILING DATE: 2000-03-10
   16 <150> PRIOR APPLICATION NUMBER: 60/059,339
   17 <151> PRIOR FILING DATE: 1997-09-19
   19 <160> NUMBER OF SEQ ID NOS: 55
   21 <170> SOFTWARE: FastSEQ for Windows Version 3.0
```

ERRORED SEQUENCES

Number of amino acids differ:
- 5 listed
- 15 shown

```
   23 <210> SEQ ID NO: 1
   24 <211> LENGTH: 5
   25 <212> TYPE: PRT
   26 <213> ORGANISM: human
   28 <400> SEQUENCE: 1
   29 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
E--> 30 1               5               10              15
  681 <210> SEQ ID NO: 54
  682 <211> LENGTH: 277
  683 <212> TYPE: PRT
  684 <213> ORGANISM: human
  686 <400> SEQUENCE: 54
  687 Met Glu His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
  688 1               5               10              15
  689 Val Leu Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Thr Arg
  690         20              25              30
  691 Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
  692         35              40              45
  693 Thr Ser His Trp Met Gln Trp Val Arg Gln Arg Pro Gly Gln Gly Leu
  694         50              55              60
  695 Glu Trp Ile Gly Thr Ile Tyr Pro Gly Asp Gly Asp Thr Arg Tyr Thr
  696 65              70              75              80
  697 Gln Asn Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Thr
  698         85              90              95
  699 Thr Ala Tyr Leu His Leu Ser Ser Leu Ser Ser Glu Asp Ser Ala Val
E--> 700         100             105             110
  701 Tyr Tyr Cys Ala Arg Asp Glu Ile Thr Thr Val Val Pro Arg Gly Phe
  702         115             120             125
  703 Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
  704         130             135             140
  705 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Leu
```

Missing amino acid numbering

```
706 145                   150                   155                   160
707  Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly Asp Thr Ile Thr
708                   165                   170                   175
709  Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp Leu Ser Trp Tyr
710              180                   185                   190
711  Gln Gln Lys Pro Gly Asn Ile Pro Gln Leu Leu Ile Tyr Lys Ala Ser
712          195                   200                    205
713  Asn Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly Arg Gly Ser Gly
714          210                   215                   220
715  Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Gly
716  225                   230                   235                   240
717  Thr Tyr Tyr Cys Gln Gln Gly Gln Ser Tyr Pro Leu Thr Phe Gly Gly
718              245                   250                   255
719  Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser
720          260                   265                   270
721  Glu Lys Asp Glu Leu
```

<210> 29   Seq. # 29
<211> 32
<212> PRT
<213> human

Missing mandatory <220> to <223> features to explain "Xaa's" in the sequence.

See #10 on the Error Summary Sheet.

<400> 29

Met Leu Phe Asn Leu Arg (Xaa)(Xaa) Leu Asn Asn Ala Ala Phe Arg His
1   5   10   15
Gly His Asn Phe Met Val Arg Asn Phe Arg Cys Gly Gln Pro Leu (Xaa)
        20   25   30

Seq # 51

```
<210> 51
<211> 837
<212> DNA
<213> human

<220>
<221> CDS
<222> (1)...(837)
```

Missing Mandatory <220> to <223> features to explain the "n" at position 505.

```
<400> 51
atg gaa cat ctg tgg ttc ttc ctt ctc ctg gtg gca gct ccc aga tgg    48
Met Glu His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5               10              15

gtc ctg tcc cag gtg caa ctg cag cag tca ggg gct gag ctg gca aga    96
Val Leu Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg
            20              25              30

cct ggg gct tca gtg aag ttg tcc tgc aag gct tct ggc tac acc ttt    144
Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35              40                  45

act agt cac tgg atg cag tgg gtg aga cag agg cct gga cag ggt ctg    192
Thr Ser His Trp Met Gln Trp Val Arg Gln Arg Pro Gly Gln Gly Leu
    50              55              60

gaa tgg att ggg act att tat cct gga gat ggt gat act agg tac act    240
Glu Trp Ile Gly Thr Ile Tyr Pro Gly Asp Gly Asp Thr Arg Tyr Thr
65              70              75              80

cag aat ttc aag ggc aag gcc aca ttg act gca gat aag tcc tcc acc    288
Gln Asn Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Thr
                85              90              95

aca gcc tac tta cac ctc agc agc ttg tca tct gaa gac tct gcg gtc    336
Thr Ala Tyr Leu His Leu Ser Ser Leu Ser Ser Glu Asp Ser Ala Val
            100             105             110

tat tat tgt gca aga gat gag att act acg gtt gta ccc cgg ggg ttt    384
Tyr Tyr Cys Ala Arg Asp Glu Ile Thr Thr Val Val Pro Arg Gly Phe
        115             120             125

gct tac tgg ggc caa ggg acc tcg gtc acc gtc tcc tca ggt ggc ggt    432
Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly
    130             135             140

ggc tcg ggc ggt ggt ggc tcg ggt ggc ggc gga tct gag ctc gtg ctc    480
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Leu
145             150             155             160

acc caa acc cca acc tcc ctg gct nnc tct ctg gga gac aga gtc acc    528
Thr Gln Thr Pro Thr Ser Leu Ala Xaa Ser Leu Gly Asp Arg Val Thr
                165             170             175

atc agt tgc agg gca agt cag gac att agc agt tat tta aac tgg tat    576
Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr
        180             185             190
```

<210> 52   Seq # 52
<211> 277
<212> PRT   *Missing mandatory <220> to <223>*
<213> human   *features to explain "Xaa" at*

                             position 169.
<400> 52
Met Glu His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1   5   10   15
Val Leu Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg
        20   25   30
Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35   40   45
Thr Ser His Trp Met Gln Trp Val Arg Gln Arg Pro Gly Gln Gly Leu
    50   55   60
Glu Trp Ile Gly Thr Ile Tyr Pro Gly Asp Gly Asp Thr Arg Tyr Thr
65   70   75   80
Gln Asn Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Thr
            85   90   95
Thr Ala Tyr Leu His Leu Ser Ser Leu Ser Ser Glu Asp Ser Ala Val
            100   105   110
Tyr Tyr Cys Ala Arg Asp Glu Ile Thr Thr Val Val Pro Arg Gly Phe
        115   120   125
Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly
        130   135   140
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Leu
145   150   155   160
Thr Gln Thr Pro Thr Ser Leu Ala Xaa Ser Leu Gly Asp Arg Val Thr
            165   170   175
Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr
            180   185   190
Gln Gln Lys Pro Asp Gly Thr Ile Lys Leu Leu Ile Tyr Tyr Thr Ser
            195   200   205
Arg Leu Tyr Ser Gly Val Pro Pro Arg Phe Ser Gly Ser Gly Ala Gly
    210   215   220
Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu Asp Phe Ala
225   230   235   240
Thr Tyr Phe Cys Gln Gln Gly Asn Val Ile Pro Tyr Thr Phe Gly Gly
            245   250   255
Gly Thr Lys Leu Glu Met Lys Arg Ala Asp Ala Ala Pro Thr Val Ser
            260   265   270
Glu Lys Asp Glu Leu
            275

```
              VERIFICATION SUMMARY              DATE: 01/04/2001
              PATENT APPLICATION:  US/09/522,727    TIME: 08:52:12

              Input Set : A:\47577.txt
              Output Set: N:\CRF3\01042001\I522727.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:30 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:15 SEQ:1
L:280 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:29
L:280 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:29
L:280 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:29
L:280 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:29
L:280 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:29
L:282 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:29
L:282 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:29
L:282 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:29
L:282 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:29
M:340 Repeated in SeqNo=29
L:522 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:51
L:522 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:51
L:523 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:51
M:340 Repeated in SeqNo=51
L:581 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:52
L:581 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:52
L:581 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:52
L:581 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:52
L:581 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:52
L:700 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:54
```